SEQUENCE LISTING

<110> Reed, John C.
      Takayama, Shinichi

<120> Novel BAG Proteins and Nucleic Acid Molecules Encoding
      Them

<130> P-LJ 3737

<140> 09/394,142
<141> 1999-09-09

<150> 09/150,489
<151> 1998-09-09

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<170> PatentIn Ver. 2.0

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Gly Gly Ala Arg Arg Pro Arg Gly Asp Arg Glu Arg Leu Gly Ser Arg
  5   10   15   20

ctg cgc gcc ctt cgg cca ggc cgg gag ccg cgc cag tcg gag ccc ccg 153
Leu Arg Ala Leu Arg Pro Gly Arg Glu Pro Arg Gln Ser Glu Pro Pro
                 25   30   35

gcc cag cgt ggt ccg cct ccc tct cgg cgt cca cct gcc cgg agt act 201
Ala Gln Arg Gly Pro Pro Pro Ser Arg Arg Pro Pro Ala Arg Ser Thr
                 40   45   50

gcc agc ggg cat gac cga ccc acc agg ggc gcc gcc gcc ggc gct cgc 249
Ala Ser Gly His Asp Arg Pro Thr Arg Gly Ala Ala Ala Gly Ala Arg

1

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agg ccg cgg atg aag aag aaa acc cgg cgc cgc tcg acc cgg agc gag    297
Arg Pro Arg Met Lys Lys Lys Thr Arg Arg Arg Ser Thr Arg Ser Glu
    70              75                  80

gag ttg acc cgg agc gag gag ttg acc ctg agt gag gaa gcg acc tgg    345
Glu Leu Thr Arg Ser Glu Glu Leu Thr Leu Ser Glu Glu Ala Thr Trp
 85              90                  95                  100

agt gaa gag gcg acc cag agt gag gag gcg acc cag ggc gaa gag atg    393
Ser Glu Glu Ala Thr Gln Ser Glu Glu Ala Thr Gln Gly Glu Glu Met
                105                 110                 115

aat cgg agc cag gag gtg acc cgg gac gag gag tcg acc cgg agc gag    441
Asn Arg Ser Gln Glu Val Thr Arg Asp Glu Glu Ser Thr Arg Ser Glu
            120                 125                 130

gag gtg acc agg gag gaa atg gcg gca gct ggg ctc acc gtg act gtc    489
Glu Val Thr Arg Glu Glu Met Ala Ala Ala Gly Leu Thr Val Thr Val
        135                 140                 145

acc cac agc aat gag aag cac gac ctt cat gtt acc tcc cag cag ggc    537
Thr His Ser Asn Glu Lys His Asp Leu His Val Thr Ser Gln Gln Gly
    150                 155                 160

agc agt gaa cca gtt gtc caa gac ctg gcc cag gtt gtt gaa gag gtc    585
Ser Ser Glu Pro Val Val Gln Asp Leu Ala Gln Val Val Glu Glu Val
165                 170                 175                 180

ata ggg gtt cca cag tct ttt cag aaa ctc ata ttt aag gga aaa tct    633
Ile Gly Val Pro Gln Ser Phe Gln Lys Leu Ile Phe Lys Gly Lys Ser
                185                 190                 195

ctg aag gaa atg gaa aca ccg ttg tca gca ctt gga ata caa gat ggt    681
Leu Lys Glu Met Glu Thr Pro Leu Ser Ala Leu Gly Ile Gln Asp Gly
                200                 205                 210

tgc cgg gtc atg tta att ggg aaa aag aac agt cca cag gaa gag gtt    729
Cys Arg Val Met Leu Ile Gly Lys Lys Asn Ser Pro Gln Glu Glu Val
            215                 220                 225

gaa cta aag aag ttg aaa cat ttg gag aag tct gtg gag aag ata gct    777
Glu Leu Lys Lys Leu Lys His Leu Glu Lys Ser Val Glu Lys Ile Ala
    230                 235                 240

gac cag ctg gaa gag ttg aat aaa gag ctt act gga atc cag cag ggt    825
Asp Gln Leu Glu Glu Leu Asn Lys Glu Leu Thr Gly Ile Gln Gln Gly
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2

ttt ctg ccc aag gat ttg caa gct gaa gct ctc tgc aaa ctt gat agg   873
Phe Leu Pro Lys Asp Leu Gln Ala Glu Ala Leu Cys Lys Leu Asp Arg
                265   270   275

aga gta aaa gcc aca ata gag cag ttt atg aag atc ttg gag gag att   921
Arg Val Lys Ala Thr Ile Glu Gln Phe Met Lys Ile Leu Glu Glu Ile
                280   285   290

gac aca ctg atc ctg cca gaa aat ttc aaa gac agt aga ttg aaa agg   969
Asp Thr Leu Ile Leu Pro Glu Asn Phe Lys Asp Ser Arg Leu Lys Arg
                295   300   305

aaa ggc ttg gta aaa aag gtt cag gca ttc cta gcc gag tgt gac aca   1017
Lys Gly Leu Val Lys Lys Val Gln Ala Phe Leu Ala Glu Cys Asp Thr
     310   315   320

gtg gag cag aac atc tgc cag gag act gag cgg ctg cag tct aca aac   1065
Val Glu Gln Asn Ile Cys Gln Glu Thr Glu Arg Leu Gln Ser Thr Asn
325   330   335   340

ttt gcc ctg gcc gag tgaggtgtag cagaaaaagg ctgtgctgcc ctgaagaatg   1120
Phe Ala Leu Ala Glu
                345

gcgccaccag ctctgccgtc tctggatcgg aatttacctg atttcttcag ggctgctggg   1180

ggcaactggc catttgccaa ttttcctact ctcacactgg ttctcaatga aaaatagtgt   1240

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Ser Glu Pro Pro Ala Gln Arg Gly Pro Pro Ser Arg Arg Pro Pro
        35   40   45

3

Ala Arg Ser Thr Ala Ser Gly His Asp Arg Pro Thr Arg Gly Ala Ala
         50   55   60

Ala Gly Ala Arg Arg Pro Arg Met Lys Lys Lys Thr Arg Arg Arg Ser
65   70   75   80

Thr Arg Ser Glu Glu Leu Thr Arg Ser Glu Glu Leu Thr Leu Ser Glu
              85   90   95

Glu Ala Thr Trp Ser Glu Glu Ala Thr Gln Ser Glu Glu Ala Thr Gln
             100   105   110

Gly Glu Glu Met Asn Arg Ser Gln Glu Val Thr Arg Asp Glu Glu Ser
            115   120   125

Thr Arg Ser Glu Glu Val Thr Arg Glu Glu Met Ala Ala Ala Gly Leu
            130   135   140

Thr Val Thr Val Thr His Ser Asn Glu Lys His Asp Leu His Val Thr
145   150   155   160

Ser Gln Gln Gly Ser Ser Glu Pro Val Val Gln Asp Leu Ala Gln Val
                165   170   175

Val Glu Glu Val Ile Gly Val Pro Gln Ser Phe Gln Lys Leu Ile Phe
            180   185   190

Lys Gly Lys Ser Leu Lys Glu Met Glu Thr Pro Leu Ser Ala Leu Gly
            195   200   205

Ile Gln Asp Gly Cys Arg Val Met Leu Ile Gly Lys Lys Asn Ser Pro
    210   215   220

Gln Glu Glu Val Glu Leu Lys Lys Leu Lys His Leu Glu Lys Ser Val
225   230   235   240

Glu Lys Ile Ala Asp Gln Leu Glu Glu Leu Asn Lys Glu Leu Thr Gly
                245   250   255

Ile Gln Gln Gly Phe Leu Pro Lys Asp Leu Gln Ala Glu Ala Leu Cys
            260   265   270

Lys Leu Asp Arg Arg Val Lys Ala Thr Ile Glu Gln Phe Met Lys Ile
    275   280   285

Leu Glu Glu Ile Asp Thr Leu Ile Leu Pro Glu Asn Phe Lys Asp Ser
    290   295   300

4

Arg Leu Lys Arg Lys Gly Leu Val Lys Lys Val Gln Ala Phe Leu Ala
305   310   315   320

Glu Cys Asp Thr Val Glu Gln Asn Ile Cys Gln Glu Thr Glu Arg Leu
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Gln Ser Thr Asn Phe Ala Leu Ala Glu
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cgccgcgttg gtgacggcga ccctgcagcc caaggagcgc tccactcgct gccgccggag 120

ggccggtgac ctcttggcta ccccgcgtcg gaggcttag atg gct cag gcg aag   174
                                             Met Ala Gln Ala Lys
                                              1   5

atc aac gct aaa gcc aac gag ggg cgc ttc tgc cgc tcc tcc tcc atg   222
Ile Asn Ala Lys Ala Asn Glu Gly Arg Phe Cys Arg Ser Ser Ser Met
                10   15   20

gct gac cgc tcc agc cgc ctg ctg gag agc ctg gac cag ctg gag ctc   270
Ala Asp Arg Ser Ser Arg Leu Leu Glu Ser Leu Asp Gln Leu Glu Leu
            25   30   35

agg gtt gaa gct ttg aga gaa gca gca act gct gtt gag caa gag aaa   318
Arg Val Glu Ala Leu Arg Glu Ala Ala Thr Ala Val Glu Gln Glu Lys
        40   45   50

gaa atc ctt ctg gaa atg atc cac agt atc caa aat agc cag gac atg   366
Glu Ile Leu Leu Glu Met Ile His Ser Ile Gln Asn Ser Gln Asp Met
        55   60   65

agg cag atc agt gac gga gaa aga gaa gaa tta aat ctg act gca aac   414
Arg Gln Ile Ser Asp Gly Glu Arg Glu Glu Leu Asn Leu Thr Ala Asn
    70   75   80   85

5

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cgt ttg atg gga aga act ctc acc gtt gaa gtg tca gta gaa aca att        462
Arg Leu Met Gly Arg Thr Leu Thr Val Glu Val Ser Val Glu Thr Ile
                90                      95                  100

aga aac ccc cag cag caa gaa tcc cta aag cat gcc aca agg att att        510
Arg Asn Pro Gln Gln Gln Glu Ser Leu Lys His Ala Thr Arg Ile Ile
                105                     110                 115

gat gag gtg gtc aat aag ttt ctg gat gat ttg gga aat gcc aag agt        558
Asp Glu Val Val Asn Lys Phe Leu Asp Asp Leu Gly Asn Ala Lys Ser
                120                     125                 130

cat tta atg tcg ctc tac agt gca tgt tca tct gag gtg cca cat ggg        606
His Leu Met Ser Leu Tyr Ser Ala Cys Ser Ser Glu Val Pro His Gly
            135                     140                 145

cca gtt gat cag aag ttt caa tcc ata gta att ggc tgt gct ctt gaa        654
Pro Val Asp Gln Lys Phe Gln Ser Ile Val Ile Gly Cys Ala Leu Glu
150                     155                     160                 165

gat cag aag aaa att aag aga aga tta gag act ctg ctt aga aat att        702
Asp Gln Lys Lys Ile Lys Arg Arg Leu Glu Thr Leu Leu Arg Asn Ile
                170                     175                 180

gaa aac tct gac aag gcc atc aag cta tta gag cat tct aaa gga gct        750
Glu Asn Ser Asp Lys Ala Ile Lys Leu Leu Glu His Ser Lys Gly Ala
                185                     190                 195

ggt tcc aaa act ctg caa caa aat gct gaa agc aga ttc aat             792
Gly Ser Lys Thr Leu Gln Gln Asn Ala Glu Ser Arg Phe Asn
                200                     205                 210


tagtcttcaa acctaagagc atttacacaa tacacaaggt gtaaaaatga taaaatacta 852

ttttaattga taactagttc tttgttaggt ataaccactt agttgacact gatagttgtt 912

tcagatgagg aaaatattcc atcaagtatc ttcagttttg tgaataacaa aactagcaat 972

attttaatta tctatctaga gatttttag attgaattct tgtcttgtac taggatctag 1032

catatttcac tattctgtgg atgaatacat agtttgtggg aaaacaaac gttcagctag 1092

gggcaaaaag catgactgct ttttcctgtc tggcatggaa tcacgcagtc accttgggca 1152

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Asp Gln Leu Glu Leu Arg Val Glu Ala Leu Arg Glu Ala Ala Thr Ala
            35   40   45

Val Glu Gln Glu Lys Glu Ile Leu Leu Glu Met Ile His Ser Ile Gln
        50   55   60

Asn Ser Gln Asp Met Arg Gln Ile Ser Asp Gly Glu Arg Glu Glu Leu
65   70   75   80

Asn Leu Thr Ala Asn Arg Leu Met Gly Arg Thr Leu Thr Val Glu Val
                85   90   95

Ser Val Glu Thr Ile Arg Asn Pro Gln Gln Glu Ser Leu Lys His
            100   105   110

Ala Thr Arg Ile Ile Asp Glu Val Val Asn Lys Phe Leu Asp Asp Leu
            115   120   125

Gly Asn Ala Lys Ser His Leu Met Ser Leu Tyr Ser Ala Cys Ser Ser
    130   135   140

Glu Val Pro His Gly Pro Val Asp Gln Lys Phe Gln Ser Ile Val Ile
145   150   155   160

Gly Cys Ala Leu Glu Asp Gln Lys Lys Ile Lys Arg Arg Leu Glu Thr
                165   170   175

Leu Leu Arg Asn Ile Glu Asn Ser Asp Lys Ala Ile Lys Leu Leu Glu
                180   185   190

His Ser Lys Gly Ala Gly Ser Lys Thr Leu Gln Gln Asn Ala Glu Ser
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Arg Phe Asn
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  1               5                  10                  15

gac cag aag ttt cta gcc ggc cag ttg cta cct ccc ttt atc tcc tcc      96
Asp Gln Lys Phe Leu Ala Gly Gln Leu Leu Pro Pro Phe Ile Ser Ser
              20                  25                  30

ttc ccc tct ggc agc gag gag gct att tcc aga cac ttc cac ccc tct     144
Phe Pro Ser Gly Ser Glu Glu Ala Ile Ser Arg His Phe His Pro Ser
          35                  40                  45

ctg gcc acg tca ccc ccg cct tta att cat aaa ggt gcc cgg cgc cgg     192
Leu Ala Thr Ser Pro Pro Pro Leu Ile His Lys Gly Ala Arg Arg Arg
      50                  55                  60

ctt ccc gga cac gtc ggc ggc gga gag ggg ccc acg gcg gcg gcc cgg     240
Leu Pro Gly His Val Gly Gly Gly Glu Gly Pro Thr Ala Ala Ala Arg
 65                  70                  75                  80

cca gag act cgg cgc ccg gag cca gcg ccc cgc acc cgc gcc cca gcg     288
Pro Glu Thr Arg Arg Pro Glu Pro Ala Pro Arg Thr Arg Ala Pro Ala
                  85                  90                  95

ggc aga ccc caa ccc agc atg agc gcc gcc acc cac tcg ccc atg atg     336
Gly Arg Pro Gln Pro Ser Met Ser Ala Ala Thr His Ser Pro Met Met
              100                 105                 110

cag gtg gcg tcc ggc aac ggt gac cgc gac cct ttg ccc ccc gga tgg     384
Gln Val Ala Ser Gly Asn Gly Asp Arg Asp Pro Leu Pro Pro Gly Trp
          115                 120                 125

gag atc aag atc gac ccg cag acc ggc tgg ccc ttc ttc gtg gac cac     432
Glu Ile Lys Ile Asp Pro Gln Thr Gly Trp Pro Phe Phe Val Asp His
      130                 135                 140

aac agc cgc acc act acg tgg aac gac ccg cgc gtg ccc tct gag ggc     480
Asn Ser Arg Thr Thr Thr Trp Asn Asp Pro Arg Val Pro Ser Glu Gly
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8

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ccc aag gag act cca tcc tct gcc aat ggc cct tcc cgg gag ggc tct    528
Pro Lys Glu Thr Pro Ser Ser Ala Asn Gly Pro Ser Arg Glu Gly Ser
                165                    170                    175

agg ctg ccg cct gct agg gaa ggc cac cct gtg tac ccc cag ctc cga    576
Arg Leu Pro Pro Ala Arg Glu Gly His Pro Val Tyr Pro Gln Leu Arg
                180                    185                    190

cca ggc tac att ccc att cct gtg ctc cat gaa ggc gct gag aac cgg    624
Pro Gly Tyr Ile Pro Ile Pro Val Leu His Glu Gly Ala Glu Asn Arg
                195                    200                    205

cag gtg cac cct ttc cat gtc tat ccc cag cct ggg atg cag cga ttc    672
Gln Val His Pro Phe His Val Tyr Pro Gln Pro Gly Met Gln Arg Phe
                210                    215                    220

cga act gag gcg gca gca gcg gct cct cag agg tcc cag tca cct ctg    720
Arg Thr Glu Ala Ala Ala Ala Ala Pro Gln Arg Ser Gln Ser Pro Leu
225                    230                    235                    240

cgg ggc atg cca gaa acc act cag cca gat aaa cag tgt gga cag gtg    768
Arg Gly Met Pro Glu Thr Thr Gln Pro Asp Lys Gln Cys Gly Gln Val
                245                    250                    255

gca gcg gcg gcg gca gcc cag ccc cca gcc tcc cac gga cct gag cgg    816
Ala Ala Ala Ala Ala Ala Gln Pro Pro Ala Ser His Gly Pro Glu Arg
                260                    265                    270

tcc cag tct cca gct gcc tct gac tgc tca tcc tca tcc tcc tcg gcc    864
Ser Gln Ser Pro Ala Ala Ser Asp Cys Ser Ser Ser Ser Ser Ser Ala
                275                    280                    285

agc ctg cct tcc tcc ggc agg agc agc ctg ggc agt cac cag ctc ccg    912
Ser Leu Pro Ser Ser Gly Arg Ser Ser Leu Gly Ser His Gln Leu Pro
                290                    295                    300

cgg ggg tac atc tcc att ccg gtg ata cac gag cag aac gtt acc cgg    960
Arg Gly Tyr Ile Ser Ile Pro Val Ile His Glu Gln Asn Val Thr Arg
305                    310                    315                    320

cca gca gcc cag ccc tcc ttc cac aaa gcc cag aag acg cac tac cca    1008
Pro Ala Ala Gln Pro Ser Phe His Lys Ala Gln Lys Thr His Tyr Pro
                325                    330                    335

gcg cag agg ggt gag tac cag acc cac cag cct gtg tac cac aag atc    1056
Ala Gln Arg Gly Glu Tyr Gln Thr His Gln Pro Val Tyr His Lys Ile
```

cag ggg gat gac tgg gag ccc cgg ccc ctg cgg gcg gca tcc ccg ttc   1104
Gln Gly Asp Asp Trp Glu Pro Arg Pro Leu Arg Ala Ala Ser Pro Phe
        355   360   365

agg tca tct gtc cag ggt gca tcg agc cgg gag ggc tca cca gcc agg   1152
Arg Ser Ser Val Gln Gly Ala Ser Ser Arg Glu Gly Ser Pro Ala Arg
     370   375   380

agc agc acg cca ctc cac tcc ccc tcg ccc atc cgt gtg cac acc gtg   1200
Ser Ser Thr Pro Leu His Ser Pro Ser Pro Ile Arg Val His Thr Val
385   390   395   400

gtc gac agg cct cag cag ccc atg acc cat cga gaa act gca cct gtt   1248
Val Asp Arg Pro Gln Gln Pro Met Thr His Arg Glu Thr Ala Pro Val
                    405   410   415

tcc cag cct gaa aac aaa cca gaa agt aag cca ggc cca gtt gga cca   1296
Ser Gln Pro Glu Asn Lys Pro Glu Ser Lys Pro Gly Pro Val Gly Pro
                420   425   430

gaa ctc cct cct gga cac atc cca att caa gtg atc cgc aaa gag gtg   1344
Glu Leu Pro Pro Gly His Ile Pro Ile Gln Val Ile Arg Lys Glu Val
                435   440   445

gat tct aaa cct gtt tcc cag aag ccc cca cct ccc tct gag aag gta   1392
Asp Ser Lys Pro Val Ser Gln Lys Pro Pro Pro Ser Glu Lys Val
                450   455   460

gag gtg aaa gtt ccc cct gct cca gtt cct tgt cct cct ccc agc cct   1440
Glu Val Lys Val Pro Pro Ala Pro Val Pro Cys Pro Pro Pro Ser Pro
465   470   475   480

ggc cct tct gct gtc ccc tct tcc ccc aag agt gtg gct aca gaa gag   1488
Gly Pro Ser Ala Val Pro Ser Ser Pro Lys Ser Val Ala Thr Glu Glu
                    485   490   495

agg gca gcc ccc agc act gcc cct gca gaa gct aca cct cca aaa cca   1536
Arg Ala Ala Pro Ser Thr Ala Pro Ala Glu Ala Thr Pro Pro Lys Pro
                500   505   510

gga gaa gcc gag gct ccc cca aaa cat cca gga gtg ctg aaa gtg gaa   1584
Gly Glu Ala Glu Ala Pro Pro Lys His Pro Gly Val Leu Lys Val Glu
                515   520   525

gcc atc ctg gag aag gtg cag ggg ctg gag cag gct gta gac aac ttt   1632
Ala Ile Leu Glu Lys Val Gln Gly Leu Glu Gln Ala Val Asp Asn Phe

```
gaa ggc aag aag act gac aaa aag tac ctg atg atc gaa gag tat ttg   1680
Glu Gly Lys Lys Thr Asp Lys Lys Tyr Leu Met Ile Glu Glu Tyr Leu
545                      550                  555                  560
```

```
acc aaa gag ctg ctg gcc ctg gat tca gtg gac ccc gag gga cga gcc   1728
Thr Lys Glu Leu Leu Ala Leu Asp Ser Val Asp Pro Glu Gly Arg Ala
                565                  570                  575
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```
gat gtg cgt cag gcc agg aga gac ggt gtc agg aag gtt cag acc atc   1776
Asp Val Arg Gln Ala Arg Arg Asp Gly Val Arg Lys Val Gln Thr Ile
                580                  585                  590
```

```
ttg gaa aaa ctt gaa cag aaa gcc att gat gtc cca ggt caa gtc cag   1824
Leu Glu Lys Leu Glu Gln Lys Ala Ile Asp Val Pro Gly Gln Val Gln
            595                  600                  605
```

```
gtc tat gaa ctc cag ccc agc aac ctt gaa gca gat cag cca ctg cag   1872
Val Tyr Glu Leu Gln Pro Ser Asn Leu Glu Ala Asp Gln Pro Leu Gln
        610                  615                  620
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```
gca atc atg gag atg ggt gcc gtg gca gca gac aag ggc aag aaa aat   1920
Ala Ile Met Glu Met Gly Ala Val Ala Ala Asp Lys Gly Lys Lys Asn
625                  630                  635                  640
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```
gct gga aat gca gaa gat ccc cac aca gaa acc cag cag cca gaa gcc   1968
Ala Gly Asn Ala Glu Asp Pro His Thr Glu Thr Gln Gln Pro Glu Ala
                645                  650                  655
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aca gca gca gcg act tca aac ccc agc agc atg aca gac acc cct ggt   2016
Thr Ala Ala Ala Thr Ser Asn Pro Ser Ser Met Thr Asp Thr Pro Gly
                660                  665                  670
```

```
aac cca gca gca ccg tagcctctgc cctgtaaaag tcagactcgg aaccgatgtg   2071
Asn Pro Ala Ala Pro
            675
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tgctttaggg attttagttg catgcatttc agagacttta ggtcagttgg ttttgattag 2131

ctgcttggta tgcagtactt gggtgaggca aacactataa agggctaaaa gggaaaatga 2191

tgcttttctt caatattctt actcttgtac aattaangaa gttgcttgtt gtttgagaag 2251

tttaaccccg ttgcttgttc tgcagccctg tcnacttggg cacccccacc acctgttagc 2311

tgtggttgtg cactgtcttt tgtagctctg gactggaggg gtagatgggg agtcaattac 2371
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ccatcacata aatatgaaac atttatcaga aatgttgcca ttttaatgag atgattttct 2431

tcatctcata attaaaatac ctgactttag agagagtaaa atgtgccagg agccatagga 2491

atatctgtat gttggatgac tttaatgcta cattth                            2528
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 1               5                  10                  15

Asp Gln Lys Phe Leu Ala Gly Gln Leu Leu Pro Pro Phe Ile Ser Ser
            20                  25                  30

Phe Pro Ser Gly Ser Glu Glu Ala Ile Ser Arg His Phe His Pro Ser
        35                  40                  45

Leu Ala Thr Ser Pro Pro Pro Leu Ile His Lys Gly Ala Arg Arg Arg
    50                  55                  60

Leu Pro Gly His Val Gly Gly Glu Gly Pro Thr Ala Ala Ala Arg
65                  70                  75                  80

Pro Glu Thr Arg Arg Pro Glu Pro Ala Pro Arg Thr Arg Ala Pro Ala
                85                  90                  95

Gly Arg Pro Gln Pro Ser Met Ser Ala Ala Thr His Ser Pro Met Met
            100                 105                 110

Gln Val Ala Ser Gly Asn Gly Asp Arg Asp Pro Leu Pro Pro Gly Trp
        115                 120                 125

Glu Ile Lys Ile Asp Pro Gln Thr Gly Trp Pro Phe Phe Val Asp His
    130                 135                 140

Asn Ser Arg Thr Thr Thr Trp Asn Asp Pro Arg Val Pro Ser Glu Gly
145                 150                 155                 160

Pro Lys Glu Thr Pro Ser Ser Ala Asn Gly Pro Ser Arg Glu Gly Ser
                165                 170                 175

Arg Leu Pro Pro Ala Arg Glu Gly His Pro Val Tyr Pro Gln Leu Arg
            180                 185                 190
```

Pro Gly Tyr Ile Pro Ile Pro Val Leu His Glu Gly Ala Glu Asn Arg
    195   200   205

Gln Val His Pro Phe His Val Tyr Pro Gln Pro Gly Met Gln Arg Phe
    210   215   220

Arg Thr Glu Ala Ala Ala Ala Ala Pro Gln Arg Ser Gln Ser Pro Leu
225   230   235   240

Arg Gly Met Pro Glu Thr Thr Gln Pro Asp Lys Gln Cys Gly Gln Val
                245   250   255

Ala Ala Ala Ala Ala Ala Gln Pro Pro Ala Ser His Gly Pro Glu Arg
                260   265   270

Ser Gln Ser Pro Ala Ala Ser Asp Cys Ser Ser Ser Ser Ser Ser Ala
        275   280   285

Ser Leu Pro Ser Ser Gly Arg Ser Ser Leu Gly Ser His Gln Leu Pro
    290   295   300

Arg Gly Tyr Ile Ser Ile Pro Val Ile His Glu Gln Asn Val Thr Arg
305   310   315   320

Pro Ala Ala Gln Pro Ser Phe His Lys Ala Gln Lys Thr His Tyr Pro
                325   330   335

Ala Gln Arg Gly Glu Tyr Gln Thr His Gln Pro Val Tyr His Lys Ile
                340   345   350

Gln Gly Asp Asp Trp Glu Pro Arg Pro Leu Arg Ala Ala Ser Pro Phe
        355   360   365

Arg Ser Ser Val Gln Gly Ala Ser Ser Arg Glu Gly Ser Pro Ala Arg
    370   375   380

Ser Ser Thr Pro Leu His Ser Pro Ser Pro Ile Arg Val His Thr Val
385   390   395   400

Val Asp Arg Pro Gln Gln Pro Met Thr His Arg Glu Thr Ala Pro Val
                405   410   415

Ser Gln Pro Glu Asn Lys Pro Glu Ser Lys Pro Gly Pro Val Gly Pro
        420   425   430

Glu Leu Pro Pro Gly His Ile Pro Ile Gln Val Ile Arg Lys Glu Val
    435   440   445

13

Asp Ser Lys Pro Val Ser Gln Lys Pro Pro Pro Ser Glu Lys Val
    450   455   460

Glu Val Lys Val Pro Pro Ala Pro Val Pro Cys Pro Pro Ser Pro
465   470   475   480

Gly Pro Ser Ala Val Pro Ser Ser Pro Lys Ser Val Ala Thr Glu Glu
            485   490   495

Arg Ala Ala Pro Ser Thr Ala Pro Ala Glu Ala Thr Pro Pro Lys Pro
            500   505   510

Gly Glu Ala Glu Ala Pro Pro Lys His Pro Gly Val Leu Lys Val Glu
        515   520   525

Ala Ile Leu Glu Lys Val Gln Gly Leu Glu Gln Ala Val Asp Asn Phe
    530   535   540

Glu Gly Lys Lys Thr Asp Lys Lys Tyr Leu Met Ile Glu Glu Tyr Leu
545   550   555   560

Thr Lys Glu Leu Leu Ala Leu Asp Ser Val Asp Pro Glu Gly Arg Ala
            565   570   575

Asp Val Arg Gln Ala Arg Arg Asp Gly Val Arg Lys Val Gln Thr Ile
            580   585   590

Leu Glu Lys Leu Glu Gln Lys Ala Ile Asp Val Pro Gly Gln Val Gln
        595   600   605

Val Tyr Glu Leu Gln Pro Ser Asn Leu Glu Ala Asp Gln Pro Leu Gln
    610   615   620

Ala Ile Met Glu Met Gly Ala Val Ala Ala Asp Lys Gly Lys Lys Asn
625   630   635   640

Ala Gly Asn Ala Glu Asp Pro His Thr Glu Thr Gln Gln Pro Glu Ala
            645   650   655

Thr Ala Ala Ala Thr Ser Asn Pro Ser Ser Met Thr Asp Thr Pro Gly
            660   665   670

Asn Pro Ala Ala Pro
        675

<210> 7

14

<211> 1010
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (323)..(1009)

<400> 7
acgatatcct gtaagaccaa gaattgcaag gccagagttt gaattcttat acaaatggag 60

cgtatggtcc aacatacccc ccaggccctg gggcaaatac tgcctcatac tcaggggctt 120

attatgcacc tggttatact cagaccagtt actccacaga agttccaagt acttaccgtt 180

catctggcaa cagcccaact ccagtctctc gttggatcta tccccagcag gactgtcaag 240

actgaagcac ccctcttaa ggggcaggtt ccaggatatc cgccttcaca gaaccctgga 300

atgaccctgc cccattatcc tt atg gag atg gta atc gta gtg ttc cac aat 352
                        Met Glu Met Val Ile Val Val Phe His Asn
                         1   5   10

cac ggc cga ctg tac gac cac aag aaa gat gcg tgg gct tct cct ggt 400
His Gly Arg Leu Tyr Asp His Lys Lys Asp Ala Trp Ala Ser Pro Gly
                 15   20   25

gct tat gga atg ggt ggc cgt tat ccc tgg cct tca tca gcg ccc tca 448
Ala Tyr Gly Met Gly Gly Arg Tyr Pro Trp Pro Ser Ser Ala Pro Ser
             30   35   40

gca cca ccc ggc aat ctc tac atg act gaa agt act tca cca tgg cct 496
Ala Pro Pro Gly Asn Leu Tyr Met Thr Glu Ser Thr Ser Pro Trp Pro
         45   50   55

agc agt ggc tct ccc cag tca ccc cct tca ccc cca gtc cag cag ccc 544
Ser Ser Gly Ser Pro Gln Ser Pro Pro Ser Pro Pro Val Gln Gln Pro
     60   65   70

aag gat tct tca tac ccc tat agc caa tca gat caa agc atg aac cgg 592
Lys Asp Ser Ser Tyr Pro Tyr Ser Gln Ser Asp Gln Ser Met Asn Arg
 75   80   85   90

cac aac ttt cct tgc agt gtc cat cag tac gaa tcc tcg ggg aca gtg 640
His Asn Phe Pro Cys Ser Val His Gln Tyr Glu Ser Ser Gly Thr Val
                 95   100   105

aac aat gat gat tca gat ctt ttg gat tcc caa gtc cag tat agt gct 688

15

```
Asn Asn Asp Asp Ser Asp Leu Leu Asp Ser Gln Val Gln Tyr Ser Ala
            110                 115                 120


gag cct cag ctg tat ggt aat gcc acc agt gac cat ccc aac aat caa    736
Glu Pro Gln Leu Tyr Gly Asn Ala Thr Ser Asp His Pro Asn Asn Gln
            125                 130                 135


gat caa agt agc agt ctt cct gaa gaa tgt gta cct tca gat gaa agt    784
Asp Gln Ser Ser Ser Leu Pro Glu Glu Cys Val Pro Ser Asp Glu Ser
            140                 145                 150


act cct ccg agt att aaa aaa atc ata cat gtg ctg gag aag gtc cag    832
Thr Pro Pro Ser Ile Lys Lys Ile Ile His Val Leu Glu Lys Val Gln
155                 160                 165                 170


tat ctt gaa caa gaa gta gaa gaa ttt gta gga aaa aag aca gac aaa    880
Tyr Leu Glu Gln Glu Val Glu Glu Phe Val Gly Lys Lys Thr Asp Lys
                    175                 180                 185


gca tac tgg ctt ctg gaa gaa atg cta acc aag gaa ctt ttg gaa ctg    928
Ala Tyr Trp Leu Leu Glu Glu Met Leu Thr Lys Glu Leu Leu Glu Leu
            190                 195                 200


gat tca gtt gaa act ggg ggc cag gac tct gta cgg cag gcc aga aaa    976
Asp Ser Val Glu Thr Gly Gly Gln Asp Ser Val Arg Gln Ala Arg Lys
            205                 210                 215


gag gct gtt tgt aag att cag gcc ata ttg gaa a                      1010
Glu Ala Val Cys Lys Ile Gln Ala Ile Leu Glu
        220                 225


<210> 8
<211> 229
<212> PRT
<213> Homo sapiens

<400> 8
Met Glu Met Val Ile Val Val Phe His Asn His Gly Arg Leu Tyr Asp
  1               5                 10                  15


His Lys Lys Asp Ala Trp Ala Ser Pro Gly Ala Tyr Gly Met Gly Gly
                20                  25                  30


Arg Tyr Pro Trp Pro Ser Ser Ala Pro Ser Ala Pro Pro Gly Asn Leu
            35                  40                  45


Tyr Met Thr Glu Ser Thr Ser Pro Trp Pro Ser Ser Gly Ser Pro Gln
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16

Ser Pro Pro Ser Pro Pro Val Gln Gln Pro Lys Asp Ser Ser Tyr Pro
    65   70   75   80

Tyr Ser Gln Ser Asp Gln Ser Met Asn Arg His Asn Phe Pro Cys Ser
                85   90   95

Val His Gln Tyr Glu Ser Ser Gly Thr Val Asn Asn Asp Asp Ser Asp
                100   105   110

Leu Leu Asp Ser Gln Val Gln Tyr Ser Ala Glu Pro Gln Leu Tyr Gly
            115   120   125

Asn Ala Thr Ser Asp His Pro Asn Asn Gln Asp Gln Ser Ser Ser Leu
            130   135   140

Pro Glu Glu Cys Val Pro Ser Asp Glu Ser Thr Pro Pro Ser Ile Lys
145   150   155   160

Lys Ile Ile His Val Leu Glu Lys Val Gln Tyr Leu Glu Gln Glu Val
                165   170   175

Glu Glu Phe Val Gly Lys Lys Thr Asp Lys Ala Tyr Trp Leu Leu Glu
            180   185   190

Glu Met Leu Thr Lys Glu Leu Leu Glu Leu Asp Ser Val Glu Thr Gly
            195   200   205

Gly Gln Asp Ser Val Arg Gln Ala Arg Lys Glu Ala Val Cys Lys Ile
    210   215   220

Gln Ala Ile Leu Glu
225

<210> 9
<211> 689
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (3)..(482)

<220>
<221> unsure
<222> (105)

17

<223> any amino acid

<400> 9

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ga gaa ata aaa aat gaa ctt ctc caa gca caa aac cct tct gaa ttg      47
   Glu Ile Lys Asn Glu Leu Leu Gln Ala Gln Asn Pro Ser Glu Leu
    1               5                  10                  15


tac ctg agc tcc aaa aca gaa ttg cag ggt tta att gga cag ttg gat     95
Tyr Leu Ser Ser Lys Thr Glu Leu Gln Gly Leu Ile Gly Gln Leu Asp
                20                  25                  30


gag gta agt ntt gaa aaa aac ccc tgc atc cgg gaa gcc agg aga aga    143
Glu Val Ser Xaa Glu Lys Asn Pro Cys Ile Arg Glu Ala Arg Arg Arg
                35                  40                  45


gca gtg atc gag gtg caa act ctg atc aca tat att gac ttg aag gag    191
Ala Val Ile Glu Val Gln Thr Leu Ile Thr Tyr Ile Asp Leu Lys Glu
            50                  55                  60


gcc ctt gag aaa aga aag ctg ttt gct tgt gag gag cac cca tcc cat    239
Ala Leu Glu Lys Arg Lys Leu Phe Ala Cys Glu Glu His Pro Ser His
        65                  70                  75


aaa gcc gtc tgg aac gtc ctt gga aac ttg tct gag atc cag gga gaa    287
Lys Ala Val Trp Asn Val Leu Gly Asn Leu Ser Glu Ile Gln Gly Glu
    80                  85                  90                  95


gtt ctt tca ttt gat gga aat cga acc gat aag aac tac atc cgg ctg    335
Val Leu Ser Phe Asp Gly Asn Arg Thr Asp Lys Asn Tyr Ile Arg Leu
                100                 105                 110


gaa gag ctg ctc acc aag cag ctg cta gcc ctg gat gct gtt gat ccg    383
Glu Glu Leu Leu Thr Lys Gln Leu Leu Ala Leu Asp Ala Val Asp Pro
            115                 120                 125


cag gga gaa gag aag tgt aag gct gcc agg aaa caa gct gtg agg ctt    431
Gln Gly Glu Glu Lys Cys Lys Ala Ala Arg Lys Gln Ala Val Arg Leu
            130                 135                 140


gcg cag aat att ctc agc tat ctc gac ctg aaa tct gat gaa tgg gag    479
Ala Gln Asn Ile Leu Ser Tyr Leu Asp Leu Lys Ser Asp Glu Trp Glu
        145                 150                 155


tac tgaaatacca gagatctcac ttttgatact gttttgcact tcatatgtgc         532
Tyr
160


ttctatgtat agagagcttt cagttcattg atttatacgt gcatatttca gtctcagtat 592
```

18

ttatgattga agcaaattct attcagtatc tgctgctttt gatgttgcaa gacaaatatc 652

attacagcac gttaactttt ccattcggat caaaaaa   689

<210> 10
<211> 160
<212> PRT
<213> Homo sapiens

<400> 10
Glu Ile Lys Asn Glu Leu Leu Gln Ala Gln Asn Pro Ser Glu Leu Tyr
 1   5   10   15

Leu Ser Ser Lys Thr Glu Leu Gln Gly Leu Ile Gly Gln Leu Asp Glu
            20   25   30

Val Ser Xaa Glu Lys Asn Pro Cys Ile Arg Glu Ala Arg Arg Arg Ala
        35   40   45

Val Ile Glu Val Gln Thr Leu Ile Thr Tyr Ile Asp Leu Lys Glu Ala
    50   55   60

Leu Glu Lys Arg Lys Leu Phe Ala Cys Glu Glu His Pro Ser His Lys
 65   70   75   80

Ala Val Trp Asn Val Leu Gly Asn Leu Ser Glu Ile Gln Gly Glu Val
                85   90   95

Leu Ser Phe Asp Gly Asn Arg Thr Asp Lys Asn Tyr Ile Arg Leu Glu
            100   105   110

Glu Leu Leu Thr Lys Gln Leu Leu Ala Leu Asp Ala Val Asp Pro Gln
            115   120   125

Gly Glu Glu Lys Cys Lys Ala Ala Arg Lys Gln Ala Val Arg Leu Ala
    130   135   140

Gln Asn Ile Leu Ser Tyr Leu Asp Leu Lys Ser Asp Glu Trp Glu Tyr
145   150   155   160

<210> 11
<211> 246
<212> DNA
<213> Caenorhabditis elegans

19

<400> 11

atgtctttcc gcctcttcgt tgaaatattt cactttcttt tccagctttt tccccatctc 60

gacctgcttt ggttttttcga gaaaaccacg ttccaaatca gcgacatctc tcaaattgag 120

atcataggct ttttgaagat tgctcaaatt atgcttctca tattgcatga gcattttgaa 180

gcccgcgtca tcaaccaaag catttttttcc acccatcaca atgatttttat cattttctttt 240

aaaatt   246

<210> 12
<211> 210
<212> PRT
<213> Caenorhabditis elegans

<400> 12

Met Lys Val Asn Val Ser Cys Ser Ser Val Gln Thr Thr Ile Asp Ile
1   5   10   15

Leu Glu Glu Asn Gln Gly Glu Asp Glu Ser Ile Leu Thr Leu Gly Gln
            20   25   30

Leu Arg Asp Arg Ile Ala Thr Asp Asn Asp Val Asp Val Glu Thr Met
        35   40   45

Lys Leu Leu His Arg Gly Lys Phe Leu Gln Gly Ala Asp Asp Val Ser
    50   55   60

Leu Ser Thr Leu Asn Phe Lys Glu Asn Asp Lys Ile Ile Val Met Gly
65   70   75   80

Gly Lys Asn Ala Leu Val Asp Asp Ala Gly Phe Lys Met Leu Met Gln
                85   90   95

Tyr Glu Lys His Asn Leu Ser Asn Leu Gln Lys Ala Tyr Asp Leu Asn
            100   105   110

Leu Arg Asp Val Ala Asp Leu Glu Arg Gly Phe Leu Glu Lys Pro Lys
        115   120   125

Gln Val Glu Met Gly Lys Lys Leu Glu Lys Lys Val Lys Tyr Phe Asn
    130   135   140

Glu Glu Ala Glu Arg His Leu Glu Thr Leu Asp Gly Met Asn Ile Ile
145   150   155   160

20

```
Thr Glu Thr Thr Pro Glu Asn Gln Ala Lys Arg Asn Arg Glu Lys Arg
              165                 170                 175

Lys Thr Leu Val Asn Gly Ile Gln Thr Leu Leu Asn Gln Asn Asp Ala
              180                 185                 190

Leu Leu Arg Arg Leu Gln Glu Tyr Gln Ser Val Leu Asn Gly Asp Ile
              195                 200                 205

Pro Glu
    210


<210> 13
<211> 1377
<212> DNA
<213> Caenorhabditis elegans

<220>
<221> CDS
<222> (1)..(1377)

<400> 13
atg cca gtc gtg aac ata cca atc aaa ata ctt ggt cag aat caa tca    48
Met Pro Val Val Asn Ile Pro Ile Lys Ile Leu Gly Gln Asn Gln Ser
  1               5                  10                  15

cat agt cga agt aac tcc tcg tct tct gtt gac aac gat cga aat caa    96
His Ser Arg Ser Asn Ser Ser Ser Ser Val Asp Asn Asp Arg Asn Gln
             20                  25                  30

cca cca cag cag cca cct caa ccg caa cca caa cag caa tct cag caa   144
Pro Pro Gln Gln Pro Pro Gln Pro Gln Pro Gln Gln Gln Ser Gln Gln
         35                  40                  45

caa tac cag cag gct cca aac gtg aat acc aat atg cat cat tcc aac   192
Gln Tyr Gln Gln Ala Pro Asn Val Asn Thr Asn Met His His Ser Asn
     50                  55                  60

gga ttc tca cct aac ttc cca tct cgt agt cct att ccg gac ttt ccc   240
Gly Phe Ser Pro Asn Phe Pro Ser Arg Ser Pro Ile Pro Asp Phe Pro
 65                  70                  75                  80

agt ttt tca tct ggg ttc cca aac gat tct gaa tgg tct tcg aat ttc   288
Ser Phe Ser Ser Gly Phe Pro Asn Asp Ser Glu Trp Ser Ser Asn Phe
                 85                  90                  95

ccg tcg ttt cca aat ttc cca agt gga ttc tca aat gga agt tct aat   336
```

```
Pro Ser Phe Pro Asn Phe Pro Ser Gly Phe Ser Asn Gly Ser Ser Asn
            100                 105                 110

ttc cct gat ttt cca aga ttc gga aga gat gga gga cta tcg cca aac    384
Phe Pro Asp Phe Pro Arg Phe Gly Arg Asp Gly Gly Leu Ser Pro Asn
            115                 120                 125

cca ccg atg caa gga tac agg aga agt cca aca cca aca tca act caa    432
Pro Pro Met Gln Gly Tyr Arg Arg Ser Pro Thr Pro Thr Ser Thr Gln
            130                 135                 140

tct cca act tct aca tta aga cgc aac tct cag cag aat caa gct cct    480
Ser Pro Thr Ser Thr Leu Arg Arg Asn Ser Gln Gln Asn Gln Ala Pro
145                 150                 155                 160

cca caa tat tct cag caa caa cca caa caa gct caa caa cgt cag aca    528
Pro Gln Tyr Ser Gln Gln Gln Pro Gln Gln Ala Gln Gln Arg Gln Thr
                    165                 170                 175

act cct ccg tca aca aaa gct tca tct cga cca cca tct cgt act cgt    576
Thr Pro Pro Ser Thr Lys Ala Ser Ser Arg Pro Pro Ser Arg Thr Arg
            180                 185                 190

gaa cca aag gaa cct gag gta ccc gag aga cca gca gtt att cca ttg    624
Glu Pro Lys Glu Pro Glu Val Pro Glu Arg Pro Ala Val Ile Pro Leu
            195                 200                 205

cca tat gag aag aag gag aaa cca ctg gag aag aaa ggt agt cgt gat    672
Pro Tyr Glu Lys Lys Glu Lys Pro Leu Glu Lys Lys Gly Ser Arg Asp
    210                 215                 220

tct gga aag ggt gat gag aac ctt gaa gag aac att gcc aag atc acg    720
Ser Gly Lys Gly Asp Glu Asn Leu Glu Glu Asn Ile Ala Lys Ile Thr
225                 230                 235                 240

atc gga aag aat aat tgc gag tta tgt ccg gaa caa gaa acg gac ggc    768
Ile Gly Lys Asn Asn Cys Glu Leu Cys Pro Glu Gln Glu Thr Asp Gly
                    245                 250                 255

gac cca tct cca cta acc tcc cca atc acc gaa gga aag cca aag aga    816
Asp Pro Ser Pro Leu Thr Ser Pro Ile Thr Glu Gly Lys Pro Lys Arg
                    260                 265                 270

gga aag aaa ctt caa cgt aat caa agt gtt gtt gat ttc aat gcc aag    864
Gly Lys Lys Leu Gln Arg Asn Gln Ser Val Val Asp Phe Asn Ala Lys
            275                 280                 285

aca att gtt act ttg gat aaa att gaa tta caa gtt gag cag ttg aga    912
```

22

```
Thr Ile Val Thr Leu Asp Lys Ile Glu Leu Gln Val Glu Gln Leu Arg
    290                 295             300

aaa aaa gct gct gaa ctc gaa atg gaa aaa gag caa att ctt cgt tct      960
Lys Lys Ala Ala Glu Leu Glu Met Glu Lys Glu Gln Ile Leu Arg Ser
305             310             315             320

cta gga gaa atc agt gtt cat aac tgc atg ttc aaa ctg gaa gaa tgt     1008
Leu Gly Glu Ile Ser Val His Asn Cys Met Phe Lys Leu Glu Glu Cys
                325             330             335

gat cgt gaa gag att gaa gca atc act gac cga ttg aca aaa aga aca     1056
Asp Arg Glu Glu Ile Glu Ala Ile Thr Asp Arg Leu Thr Lys Arg Thr
            340             345             350

aag aca gtt caa gtt gtt gtc gaa act cca cga aat gaa gaa cag aaa     1104
Lys Thr Val Gln Val Val Val Glu Thr Pro Arg Asn Glu Glu Gln Lys
        355             360             365

aaa gca ctg gaa gat gca act ttg atg atc gat gaa gtc gga gaa atg     1152
Lys Ala Leu Glu Asp Ala Thr Leu Met Ile Asp Glu Val Gly Glu Met
    370             375             380

atg cat tcg aat att gaa aag gct aag ctg tgc cta caa acc tac atg     1200
Met His Ser Asn Ile Glu Lys Ala Lys Leu Cys Leu Gln Thr Tyr Met
385             390             395             400

aac gcc tgt tcg tac gaa gaa act gct gga gcc acc tgc caa aac ttc     1248
Asn Ala Cys Ser Tyr Glu Glu Thr Ala Gly Ala Thr Cys Gln Asn Phe
                405             410             415

ttg aag atc ata att cag tgc gct gct gat gat cag aaa cgc atc aag     1296
Leu Lys Ile Ile Ile Gln Cys Ala Ala Asp Asp Gln Lys Arg Ile Lys
            420             425             430

cgt cgt ctg gaa aat ctg atg tct caa att gag aat gct gag aga acg     1344
Arg Arg Leu Glu Asn Leu Met Ser Gln Ile Glu Asn Ala Glu Arg Thr
            435             440             445

aaa gca gat ttg atg gat gat caa agc gaa tag                         1377
Lys Ala Asp Leu Met Asp Asp Gln Ser Glu
    450             455


<210> 14
<211> 458
<212> PRT
<213> Caenorhabditis elegans
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<400> 14

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Met Pro Val Val Asn Ile Pro Ile Lys Ile Leu Gly Gln Asn Gln Ser
 1               5                  10                  15

His Ser Arg Ser Asn Ser Ser Ser Ser Val Asp Asn Asp Arg Asn Gln
                20                  25                  30

Pro Pro Gln Gln Pro Pro Gln Pro Gln Pro Gln Gln Gln Ser Gln Gln
            35                  40                  45

Gln Tyr Gln Gln Ala Pro Asn Val Asn Thr Asn Met His His Ser Asn
        50                  55                  60

Gly Phe Ser Pro Asn Phe Pro Ser Arg Ser Pro Ile Pro Asp Phe Pro
 65                  70                  75                  80

Ser Phe Ser Ser Gly Phe Pro Asn Asp Ser Glu Trp Ser Ser Asn Phe
                85                  90                  95

Pro Ser Phe Pro Asn Phe Pro Ser Gly Phe Ser Asn Gly Ser Ser Asn
            100                 105                 110

Phe Pro Asp Phe Pro Arg Phe Gly Arg Asp Gly Gly Leu Ser Pro Asn
            115                 120                 125

Pro Pro Met Gln Gly Tyr Arg Arg Ser Pro Thr Pro Thr Ser Thr Gln
        130                 135                 140

Ser Pro Thr Ser Thr Leu Arg Arg Asn Ser Gln Gln Asn Gln Ala Pro
145                 150                 155                 160

Pro Gln Tyr Ser Gln Gln Pro Gln Gln Ala Gln Gln Arg Gln Thr
            165                 170                 175

Thr Pro Pro Ser Thr Lys Ala Ser Ser Arg Pro Pro Ser Arg Thr Arg
            180                 185                 190

Glu Pro Lys Glu Pro Glu Val Pro Glu Arg Pro Ala Val Ile Pro Leu
            195                 200                 205

Pro Tyr Glu Lys Lys Glu Lys Pro Leu Glu Lys Lys Gly Ser Arg Asp
        210                 215                 220

Ser Gly Lys Gly Asp Glu Asn Leu Glu Glu Asn Ile Ala Lys Ile Thr
225                 230                 235                 240

Ile Gly Lys Asn Asn Cys Glu Leu Cys Pro Glu Gln Glu Thr Asp Gly
```

24

Asp Pro Ser Pro Leu Thr Ser Pro Ile Thr Glu Gly Lys Pro Lys Arg
            260   265   270

Gly Lys Lys Leu Gln Arg Asn Gln Ser Val Val Asp Phe Asn Ala Lys
        275   280   285

Thr Ile Val Thr Leu Asp Lys Ile Glu Leu Gln Val Glu Gln Leu Arg
    290   295   300

Lys Lys Ala Ala Glu Leu Glu Met Glu Lys Glu Gln Ile Leu Arg Ser
305   310   315   320

Leu Gly Glu Ile Ser Val His Asn Cys Met Phe Lys Leu Glu Glu Cys
                325   330   335

Asp Arg Glu Glu Ile Glu Ala Ile Thr Asp Arg Leu Thr Lys Arg Thr
            340   345   350

Lys Thr Val Gln Val Val Val Glu Thr Pro Arg Asn Glu Glu Gln Lys
        355   360   365

Lys Ala Leu Glu Asp Ala Thr Leu Met Ile Asp Glu Val Gly Glu Met
    370   375   380

Met His Ser Asn Ile Glu Lys Ala Lys Leu Cys Leu Gln Thr Tyr Met
385   390   395   400

Asn Ala Cys Ser Tyr Glu Glu Thr Ala Gly Ala Thr Cys Gln Asn Phe
                405   410   415

Leu Lys Ile Ile Ile Gln Cys Ala Ala Asp Asp Gln Lys Arg Ile Lys
            420   425   430

Arg Arg Leu Glu Asn Leu Met Ser Gln Ile Glu Asn Ala Glu Arg Thr
        435   440   445

Lys Ala Asp Leu Met Asp Asp Gln Ser Glu
    450   455

<210> 15
<211> 588
<212> DNA
<213> Schizosaccharomyces pombe

<220>

25

<221> CDS
<222> (1)..(588)

<400> 15
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atg tca gaa aag act agc aca gtt aca ata cac tat gga aat cag cga    48
Met Ser Glu Lys Thr Ser Thr Val Thr Ile His Tyr Gly Asn Gln Arg
  1               5                  10                  15

ttt ccg gta gca gtc aat cta aat gag acg tta agt gaa ctg att gat    96
Phe Pro Val Ala Val Asn Leu Asn Glu Thr Leu Ser Glu Leu Ile Asp
             20                  25                  30

gat tta ctt gaa acg act gag att tct gag aag aaa gtc aag ctt ttt   144
Asp Leu Leu Glu Thr Thr Glu Ile Ser Glu Lys Lys Val Lys Leu Phe
         35                  40                  45

tac gct ggc aag cgt tta aaa gac aaa aaa gcc tcg tta tca aaa ttg   192
Tyr Ala Gly Lys Arg Leu Lys Asp Lys Lys Ala Ser Leu Ser Lys Leu
     50                  55                  60

ggt tta aaa aat cat agt aaa att cta tgt ata aga cca cat aag caa   240
Gly Leu Lys Asn His Ser Lys Ile Leu Cys Ile Arg Pro His Lys Gln
 65                  70                  75                  80

caa cga ggt tcc aag gaa aaa gac acg gtt gag ccc gct ccg aaa gcg   288
Gln Arg Gly Ser Lys Glu Lys Asp Thr Val Glu Pro Ala Pro Lys Ala
                 85                  90                  95

gaa gcg gag aat cct gta ttt tcg cgt att tct gga gaa ata aaa gcc   336
Glu Ala Glu Asn Pro Val Phe Ser Arg Ile Ser Gly Glu Ile Lys Ala
             100                 105                 110

atc gat cag tat gtt gac aaa gaa ctt tcc ccc atg tac gac aat tac   384
Ile Asp Gln Tyr Val Asp Lys Glu Leu Ser Pro Met Tyr Asp Asn Tyr
         115                 120                 125

gta aat aaa ccg tcg aac gat cca aag cag aaa aac aaa cag aaa cta   432
Val Asn Lys Pro Ser Asn Asp Pro Lys Gln Lys Asn Lys Gln Lys Leu
     130                 135                 140

atg ata agt gaa cta ctt tta caa cag ctt tta aaa ttg gat gga gtt   480
Met Ile Ser Glu Leu Leu Leu Gln Gln Leu Leu Lys Leu Asp Gly Val
145                 150                 155                 160

gac gta ctg ggc agc gag aaa ttg cgt ttt gaa cgg aag caa ctt gtt   528
Asp Val Leu Gly Ser Glu Lys Leu Arg Phe Glu Arg Lys Gln Leu Val
                 165                 170                 175
```

```
tct aag atc caa aaa atg ttg gat cac gtt gac caa aca agc caa gaa      576
Ser Lys Ile Gln Lys Met Leu Asp His Val Asp Gln Thr Ser Gln Glu
        180             185             190

gtg gcc gca tag                                                      588
Val Ala Ala
        195


<210> 16
<211> 195
<212> PRT
<213> Schizosaccharomyces pombe

<400> 16
Met Ser Glu Lys Thr Ser Thr Val Thr Ile His Tyr Gly Asn Gln Arg
 1               5                  10                  15

Phe Pro Val Ala Val Asn Leu Asn Glu Thr Leu Ser Glu Leu Ile Asp
            20                  25                  30

Asp Leu Leu Glu Thr Thr Glu Ile Ser Glu Lys Lys Val Lys Leu Phe
        35                  40                  45

Tyr Ala Gly Lys Arg Leu Lys Asp Lys Lys Ala Ser Leu Ser Lys Leu
        50                  55                  60

Gly Leu Lys Asn His Ser Lys Ile Leu Cys Ile Arg Pro His Lys Gln
 65                  70                  75                  80

Gln Arg Gly Ser Lys Glu Lys Asp Thr Val Glu Pro Ala Pro Lys Ala
                85                  90                  95

Glu Ala Glu Asn Pro Val Phe Ser Arg Ile Ser Gly Glu Ile Lys Ala
                100                 105                 110

Ile Asp Gln Tyr Val Asp Lys Glu Leu Ser Pro Met Tyr Asp Asn Tyr
            115                 120                 125

Val Asn Lys Pro Ser Asn Asp Pro Lys Gln Lys Asn Lys Gln Lys Leu
        130                 135                 140

Met Ile Ser Glu Leu Leu Leu Gln Gln Leu Leu Lys Leu Asp Gly Val
145                 150                 155                 160

Asp Val Leu Gly Ser Glu Lys Leu Arg Phe Glu Arg Lys Gln Leu Val
                165                 170                 175
```

27

Ser Lys Ile Gln Lys Met Leu Asp His Val Asp Gln Thr Ser Gln Glu
        180   185   190

Val Ala Ala
        195

<210> 17
<211> 621
<212> DNA
<213> Schizosaccharomyces pombe

<220>
<221> CDS
<222> (1)..(621)

<400> 17
atg tct ttt ttt acc cag ttg tgt tct atg gat aaa aaa tat tgg atc   48
Met Ser Phe Phe Thr Gln Leu Cys Ser Met Asp Lys Lys Tyr Trp Ile
1   5   10   15

tct cta gct gta ttg tca gtt act gtt ttg att agc gca tta ttg aaa   96
Ser Leu Ala Val Leu Ser Val Thr Val Leu Ile Ser Ala Leu Leu Lys
             20   25   30

aag aga gct act gaa acc gaa gat att gtc gtt gtt cat tac gat ggc   144
Lys Arg Ala Thr Glu Thr Glu Asp Ile Val Val Val His Tyr Asp Gly
             35   40   45

gaa aag ttg aat ttt gtg ttg cga caa cca agg ctg aat atg gtt tct   192
Glu Lys Leu Asn Phe Val Leu Arg Gln Pro Arg Leu Asn Met Val Ser
     50   55   60

tac act agt ttt ctt cgt cgc gtg tgc aac gca ttt tca gta atg ccc   240
Tyr Thr Ser Phe Leu Arg Arg Val Cys Asn Ala Phe Ser Val Met Pro
65   70   75   80

gac aaa gcg tct ctc aag tta aac ggg gtg acc ctc aag gat ggt tca   288
Asp Lys Ala Ser Leu Lys Leu Asn Gly Val Thr Leu Lys Asp Gly Ser
             85   90   95

ctt tcc gac caa aat gtg caa aat gga agt gaa tta gag ctc gaa tta   336
Leu Ser Asp Gln Asn Val Gln Asn Gly Ser Glu Leu Glu Leu Glu Leu
             100   105   110

ccc aaa ctg agc ccg gca atg caa caa att gaa gca tat ata gat gag   384
Pro Lys Leu Ser Pro Ala Met Gln Gln Ile Glu Ala Tyr Ile Asp Glu
             115   120   125

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ctt caa cag gat ctc gtc cct aaa att gaa gcc ttc tgc caa tcg tct    432
Leu Gln Gln Asp Leu Val Pro Lys Ile Glu Ala Phe Cys Gln Ser Ser
    130                 135                 140

ccc gct tcg gca caa gat gtt caa gat ttg cat aca cgc ctt agt gaa    480
Pro Ala Ser Ala Gln Asp Val Gln Asp Leu His Thr Arg Leu Ser Glu
145                 150                 155                 160

aca ttg ttg gct agg atg ata aaa tta gat gct gtt aat gtt gaa gac    528
Thr Leu Leu Ala Arg Met Ile Lys Leu Asp Ala Val Asn Val Glu Asp
                165                 170                 175

gac cca gaa gct cgt ctt aaa aga aaa gaa gct att cgt tta tct caa    576
Asp Pro Glu Ala Arg Leu Lys Arg Lys Glu Ala Ile Arg Leu Ser Gln
                180                 185                 190

caa tat ttg agt aaa cta gat tcc acc aag aat caa aac aaa tga        621
Gln Tyr Leu Ser Lys Leu Asp Ser Thr Lys Asn Gln Asn Lys
            195                 200                 205


<210> 18
<211> 206
<212> PRT
<213> Schizosaccharomyces pombe

<400> 18
Met Ser Phe Phe Thr Gln Leu Cys Ser Met Asp Lys Lys Tyr Trp Ile
  1               5                   10                  15

Ser Leu Ala Val Leu Ser Val Thr Val Leu Ile Ser Ala Leu Leu Lys
            20                  25                  30

Lys Arg Ala Thr Glu Thr Glu Asp Ile Val Val Val His Tyr Asp Gly
            35                  40                  45

Glu Lys Leu Asn Phe Val Leu Arg Gln Pro Arg Leu Asn Met Val Ser
        50                  55                  60

Tyr Thr Ser Phe Leu Arg Arg Val Cys Asn Ala Phe Ser Val Met Pro
 65                 70                  75                  80

Asp Lys Ala Ser Leu Lys Leu Asn Gly Val Thr Leu Lys Asp Gly Ser
                85                  90                  95

Leu Ser Asp Gln Asn Val Gln Asn Gly Ser Glu Leu Glu Leu Glu Leu
            100                 105                 110
```

29

```
Pro Lys Leu Ser Pro Ala Met Gln Gln Ile Glu Ala Tyr Ile Asp Glu
        115                 120                 125

Leu Gln Gln Asp Leu Val Pro Lys Ile Glu Ala Phe Cys Gln Ser Ser
    130                 135                 140

Pro Ala Ser Ala Gln Asp Val Gln Asp Leu His Thr Arg Leu Ser Glu
145                 150                 155                 160

Thr Leu Leu Ala Arg Met Ile Lys Leu Asp Ala Val Asn Val Glu Asp
                165                 170                 175

Asp Pro Glu Ala Arg Leu Lys Arg Lys Glu Ala Ile Arg Leu Ser Gln
            180                 185                 190

Gln Tyr Leu Ser Lys Leu Asp Ser Thr Lys Asn Gln Asn Lys
        195                 200                 205


<210> 19
<211> 2534
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (307)..(2034)

<400> 19
gcggagctcc gcatccaacc ccgggccgcg gccaacttct ctggactgga ccagaagttt  60

ctagccggcc agttgctacc tccctttatc tcctccttcc cctctggcag cgaggaggct  120

atttccagac acttccaccc ctctctggcc acgtcacccc cgcctttaat tcataaaggt  180

gcccggcgcc ggcttcccgg acacgtcggc ggcggagagg ggcccacggc ggcggcccgg  240

ccagagactc ggcgcccgga gccagcgccc cgcacccgcg ccccagcggg cagacgccaa  300

cccagc atg agc gcc gcc acc cac tcg ccc atg atg cag gtg gcg tcc     348
        Met Ser Ala Ala Thr His Ser Pro Met Met Gln Val Ala Ser
         1               5                   10

ggc aac ggt gac cgc gac cct ttg ccc ccc gga tgg gag atc aag atc   396
Gly Asn Gly Asp Arg Asp Pro Leu Pro Pro Gly Trp Glu Ile Lys Ile
 15                  20                  25                  30
```

```
gac ccg cag acc ggc tgg ccc ttc ttc gtg gac cac aac agc cgc acc    444
Asp Pro Gln Thr Gly Trp Pro Phe Phe Val Asp His Asn Ser Arg Thr
                35                  40                  45


act acg tgg aac gac ccg cgc gtg ccc tct gag ggc ccc aag gag act    492
Thr Thr Trp Asn Asp Pro Arg Val Pro Ser Glu Gly Pro Lys Glu Thr
                50                  55                  60


cca tcc tct gcc aat ggc cct tcc cgg gag ggc tct agg ctg ccg cct    540
Pro Ser Ser Ala Asn Gly Pro Ser Arg Glu Gly Ser Arg Leu Pro Pro
            65                  70                  75


gct agg gaa ggc cac cct gtg tac ccc cag ctc cga cca ggc tac att    588
Ala Arg Glu Gly His Pro Val Tyr Pro Gln Leu Arg Pro Gly Tyr Ile
        80                  85                  90


ccc att cct gtg ctc cat gaa ggc gct gag aac cgg cag gtg cac cct    636
Pro Ile Pro Val Leu His Glu Gly Ala Glu Asn Arg Gln Val His Pro
    95                  100                 105                 110


ttc cat gtc tat ccc cag cct ggg atg cag cga ttc cga act gag gcg    684
Phe His Val Tyr Pro Gln Pro Gly Met Gln Arg Phe Arg Thr Glu Ala
                115                 120                 125


gca gca gcg gct cct cag agg tcc cag tca cct ctg cgg ggc atg cca    732
Ala Ala Ala Ala Pro Gln Arg Ser Gln Ser Pro Leu Arg Gly Met Pro
            130                 135                 140


gaa acc act cag cca gat aaa cag tgt gga cag gtg gca gcg gcg gcg    780
Glu Thr Thr Gln Pro Asp Lys Gln Cys Gly Gln Val Ala Ala Ala Ala
            145                 150                 155


gca gcc cag ccc cca gcc tcc cac gga cct gag cgg tcc cag tct cca    828
Ala Ala Gln Pro Pro Ala Ser His Gly Pro Glu Arg Ser Gln Ser Pro
    160                 165                 170


gct gcc tct gac tgc tca tcc tca tcc tcc tcg gcc agc ctg cct tcc    876
Ala Ala Ser Asp Cys Ser Ser Ser Ser Ser Ser Ala Ser Leu Pro Ser
175                 180                 185                 190


tcc ggc agg agc agc ctg ggc agt cac cag ctc ccg cgg ggg tac atc    924
Ser Gly Arg Ser Ser Leu Gly Ser His Gln Leu Pro Arg Gly Tyr Ile
                195                 200                 205


tcc att ccg gtg ata cac gag cag aac gtt acc cgg cca gca gcc cag    972
Ser Ile Pro Val Ile His Glu Gln Asn Val Thr Arg Pro Ala Ala Gln
            210                 215                 220
```

```
ccc tcc ttc cac aaa gcc cag aag acg cac tac cca gcg cag agg ggt    1020
Pro Ser Phe His Lys Ala Gln Lys Thr His Tyr Pro Ala Gln Arg Gly
            225             230             235

gag tac cag acc cac cag cct gtg tac cac aag atc cag ggg gat gac    1068
Glu Tyr Gln Thr His Gln Pro Val Tyr His Lys Ile Gln Gly Asp Asp
        240             245             250

tgg gag ccc cgg ccc ctg cgg gcg gca tcc ccg ttc agg tca tct gtc    1116
Trp Glu Pro Arg Pro Leu Arg Ala Ala Ser Pro Phe Arg Ser Ser Val
255             260             265             270

cag ggt gca tcg agc cgg gag ggc tca cca gcc agg agc agc acg cca    1164
Gln Gly Ala Ser Ser Arg Glu Gly Ser Pro Ala Arg Ser Ser Thr Pro
            275             280             285

ctc cac tcc ccc tcg ccc atc cgt gtg cac acc gtg gtc gac agg cct    1212
Leu His Ser Pro Ser Pro Ile Arg Val His Thr Val Val Asp Arg Pro
            290             295             300

cag cag ccc atg acc cat cga gaa act gca cct gtt tcc cag cct gaa    1260
Gln Gln Pro Met Thr His Arg Glu Thr Ala Pro Val Ser Gln Pro Glu
        305             310             315

aac aaa cca gaa agt aag cca ggc cca gtt gga cca gaa ctc cct cct    1308
Asn Lys Pro Glu Ser Lys Pro Gly Pro Val Gly Pro Glu Leu Pro Pro
    320             325             330

gga cac atc cca att caa gtg atc cgc aaa gag gtg gat tct aaa cct    1356
Gly His Ile Pro Ile Gln Val Ile Arg Lys Glu Val Asp Ser Lys Pro
335             340             345             350

gtt tcc cag aag ccc cca cct ccc tct gag aag gta gag gtg aaa gtt    1404
Val Ser Gln Lys Pro Pro Pro Pro Ser Glu Lys Val Glu Val Lys Val
            355             360             365

ccc cct gct cca gtt cct tgt cct cct ccc agc cct ggc cct tct gct    1452
Pro Pro Ala Pro Val Pro Cys Pro Pro Pro Ser Pro Gly Pro Ser Ala
            370             375             380

gtc ccc tct tcc ccc aag agt gtg gct aca gaa gag agg gca gcc ccc    1500
Val Pro Ser Ser Pro Lys Ser Val Ala Thr Glu Glu Arg Ala Ala Pro
        385             390             395

agc act gcc cct gca gaa gct aca cct cca aaa cca gga gaa gcc gag    1548
Ser Thr Ala Pro Ala Glu Ala Thr Pro Pro Lys Pro Gly Glu Ala Glu
    400             405             410
```

32

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gct ccc cca aaa cat cca gga gtg ctg aaa gtg gaa gcc atc ctg gag   1596
Ala Pro Pro Lys His Pro Gly Val Leu Lys Val Glu Ala Ile Leu Glu
415             420             425             430

aag gtg cag ggg ctg gag cag gct gta gac aac ttt gaa ggc aag aag   1644
Lys Val Gln Gly Leu Glu Gln Ala Val Asp Asn Phe Glu Gly Lys Lys
                435             440             445

act gac aaa aag tac ctg atg atc gaa gag tat ttg acc aaa gag ctg   1692
Thr Asp Lys Lys Tyr Leu Met Ile Glu Glu Tyr Leu Thr Lys Glu Leu
            450             455             460

ctg gcc ctg gat tca gtg gac ccc gag gga cga gcc gat gtg cgt cag   1740
Leu Ala Leu Asp Ser Val Asp Pro Glu Gly Arg Ala Asp Val Arg Gln
        465             470             475

gcc agg aga gac ggt gtc agg aag gtt cag acc atc ttg gaa aaa ctt   1788
Ala Arg Arg Asp Gly Val Arg Lys Val Gln Thr Ile Leu Glu Lys Leu
        480             485             490

gaa cag aaa gcc att gat gtc cca ggt caa gtc cag gtc tat gaa ctc   1836
Glu Gln Lys Ala Ile Asp Val Pro Gly Gln Val Gln Val Tyr Glu Leu
495             500             505             510

cag ccc agc aac ctt gaa gca gat cag cca ctg cag gca atc atg gag   1884
Gln Pro Ser Asn Leu Glu Ala Asp Gln Pro Leu Gln Ala Ile Met Glu
                515             520             525

atg ggt gcc gtg gca gca gac aag ggc aag aaa aat gct gga aat gca   1932
Met Gly Ala Val Ala Ala Asp Lys Gly Lys Lys Asn Ala Gly Asn Ala
                530             535             540

gaa gat ccc cac aca gaa acc cag cag cca gaa gcc aca gca gca gcg   1980
Glu Asp Pro His Thr Glu Thr Gln Gln Pro Glu Ala Thr Ala Ala Ala
            545             550             555

act tca aac ccc agc agc atg aca gac acc cct ggt aac cca gca gca   2028
Thr Ser Asn Pro Ser Ser Met Thr Asp Thr Pro Gly Asn Pro Ala Ala
        560             565             570

ccg tag cctctgccct gtaaaaatca gactcggaac cgatgtgtgc tttagggaat   2084
Pro
575


tttaagttgc atgcatttca gagactttaa gtcagttggt ttttattagc tgcttggtat 2144

gcagtaactt gggtggaggc aaaacactaa taaaagggct aaaaaggaaa atgatgcttt 2204
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tcttctatat tcttactctg tacaaataaa gaagttgctt gttgtttgag aagtttaacc 2264

ccgttgcttg ttctgcagcc ctgtctactt gggcaccccc accacctgtt agctgtggtt 2324

gtgcactgtc ttttgtagct ctggactgga ggggtagatg gggagtcaat tacccatcac 2384

ataaatatga aacatttatc agaaatgttg ccattttaat gagatgattt tcttcatctc 2444

ataattaaaa tacctgactt tagagagagt aaaatgtgcc aggagccata ggaatatctg 2504

tatgttggat gactttaatg ctacattttc   2534

<210> 20
<211> 575
<212> PRT
<213> Homo sapiens

<400> 20
Met Ser Ala Ala Thr His Ser Pro Met Met Gln Val Ala Ser Gly Asn
 1   5   10   15

Gly Asp Arg Asp Pro Leu Pro Pro Gly Trp Glu Ile Lys Ile Asp Pro
            20   25   30

Gln Thr Gly Trp Pro Phe Phe Val Asp His Asn Ser Arg Thr Thr Thr
         35   40   45

Trp Asn Asp Pro Arg Val Pro Ser Glu Gly Pro Lys Glu Thr Pro Ser
    50   55   60

Ser Ala Asn Gly Pro Ser Arg Glu Gly Ser Arg Leu Pro Pro Ala Arg
65   70   75   80

Glu Gly His Pro Val Tyr Pro Gln Leu Arg Pro Gly Tyr Ile Pro Ile
                85   90   95

Pro Val Leu His Glu Gly Ala Glu Asn Arg Gln Val His Pro Phe His
            100   105   110

Val Tyr Pro Gln Pro Gly Met Gln Arg Phe Arg Thr Glu Ala Ala Ala
         115   120   125

Ala Ala Pro Gln Arg Ser Gln Ser Pro Leu Arg Gly Met Pro Glu Thr
    130   135   140

Thr Gln Pro Asp Lys Gln Cys Gly Gln Val Ala Ala Ala Ala Ala Ala
145   150   155   160

34

Gln Pro Pro Ala Ser His Gly Pro Glu Arg Ser Gln Ser Pro Ala Ala
            165   170   175

Ser Asp Cys Ser Ser Ser Ser Ser Ser Ala Ser Leu Pro Ser Ser Gly
            180   185   190

Arg Ser Ser Leu Gly Ser His Gln Leu Pro Arg Gly Tyr Ile Ser Ile
            195   200   205

Pro Val Ile His Glu Gln Asn Val Thr Arg Pro Ala Ala Gln Pro Ser
    210   215   220

Phe His Lys Ala Gln Lys Thr His Tyr Pro Ala Gln Arg Gly Glu Tyr
225   230   235   240

Gln Thr His Gln Pro Val Tyr His Lys Ile Gln Gly Asp Asp Trp Glu
            245   250   255

Pro Arg Pro Leu Arg Ala Ala Ser Pro Phe Arg Ser Ser Val Gln Gly
            260   265   270

Ala Ser Ser Arg Glu Gly Ser Pro Ala Arg Ser Ser Thr Pro Leu His
            275   280   285

Ser Pro Ser Pro Ile Arg Val His Thr Val Val Asp Arg Pro Gln Gln
    290   295   300

Pro Met Thr His Arg Glu Thr Ala Pro Val Ser Gln Pro Glu Asn Lys
305   310   315   320

Pro Glu Ser Lys Pro Gly Pro Val Gly Pro Glu Leu Pro Pro Gly His
            325   330   335

Ile Pro Ile Gln Val Ile Arg Lys Glu Val Asp Ser Lys Pro Val Ser
            340   345   350

Gln Lys Pro Pro Pro Pro Ser Glu Lys Val Glu Val Lys Val Pro Pro
            355   360   365

Ala Pro Val Pro Cys Pro Pro Pro Ser Pro Gly Pro Ser Ala Val Pro
    370   375   380

Ser Ser Pro Lys Ser Val Ala Thr Glu Glu Arg Ala Ala Pro Ser Thr
385   390   395   400

Ala Pro Ala Glu Ala Thr Pro Pro Lys Pro Gly Glu Ala Glu Ala Pro
            405   410   415

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Pro Lys His Pro Gly Val Leu Lys Val Glu Ala Ile Leu Glu Lys Val
         420                   425                   430

Gln Gly Leu Glu Gln Ala Val Asp Asn Phe Glu Gly Lys Lys Thr Asp
         435                   440                   445

Lys Lys Tyr Leu Met Ile Glu Glu Tyr Leu Thr Lys Glu Leu Leu Ala
         450                   455                   460

Leu Asp Ser Val Asp Pro Glu Gly Arg Ala Asp Val Arg Gln Ala Arg
465                   470                   475                   480

Arg Asp Gly Val Arg Lys Val Gln Thr Ile Leu Glu Lys Leu Glu Gln
                  485                   490                   495

Lys Ala Ile Asp Val Pro Gly Gln Val Gln Val Tyr Glu Leu Gln Pro
                  500                   505                   510

Ser Asn Leu Glu Ala Asp Gln Pro Leu Gln Ala Ile Met Glu Met Gly
         515                   520                   525

Ala Val Ala Ala Asp Lys Gly Lys Lys Asn Ala Gly Asn Ala Glu Asp
         530                   535                   540

Pro His Thr Glu Thr Gln Gln Pro Glu Ala Thr Ala Ala Ala Thr Ser
545                   550                   555                   560

Asn Pro Ser Ser Met Thr Asp Thr Pro Gly Asn Pro Ala Ala Pro
                  565                   570                   575


<210> 21
<211> 1966
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (43)..(1416)

<400> 21
cggtgggagc ggggcgggaa gcgcttcagg gcagcggatc cc atg tcg gcc ctg      54
                                                Met Ser Ala Leu
                                                 1

agg cgc tcg ggc tac ggc ccc agt gac ggt ccg tcc tac ggc cgc tac    102
Arg Arg Ser Gly Tyr Gly Pro Ser Asp Gly Pro Ser Tyr Gly Arg Tyr
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36

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tac ggg cct ggg ggt gga gat gtg ccg gta cac cca cct cca ccc tta    150
Tyr Gly Pro Gly Gly Gly Asp Val Pro Val His Pro Pro Pro Leu
                25                      30                      35


tat cct ctt cgc cct gaa cct ccc cag cct ccc att tcc tgg cgg gtg    198
Tyr Pro Leu Arg Pro Glu Pro Pro Gln Pro Pro Ile Ser Trp Arg Val
            40                      45                  50


cgc ggg ggc ggc ccg gcg gag acc acc tgg ctg gga gaa ggc gga gga    246
Arg Gly Gly Gly Pro Ala Glu Thr Thr Trp Leu Gly Glu Gly Gly Gly
        55                      60                      65


ggc gat ggc tac tat ccc tcg gga ggc gcc tgg cca gag cct ggt cga    294
Gly Asp Gly Tyr Tyr Pro Ser Gly Gly Ala Trp Pro Glu Pro Gly Arg
    70                      75                      80


gcc gga gga agc cac cag gag cag cca cca tat cct agc tac aat tct    342
Ala Gly Gly Ser His Gln Glu Gln Pro Pro Tyr Pro Ser Tyr Asn Ser
85                      90                      95                  100


aac tat tgg aat tct act gcg aga tct agg gct cct tac cca agt aca    390
Asn Tyr Trp Asn Ser Thr Ala Arg Ser Arg Ala Pro Tyr Pro Ser Thr
                105                     110                     115


tat cct gta aga cca gaa ttg caa ggc cag agt ttg aat tct tat aca    438
Tyr Pro Val Arg Pro Glu Leu Gln Gly Gln Ser Leu Asn Ser Tyr Thr
            120                     125                     130


aat gga gcg tat ggt cca aca tac ccc cca ggc cct ggg gca aat act    486
Asn Gly Ala Tyr Gly Pro Thr Tyr Pro Pro Gly Pro Gly Ala Asn Thr
    135                     140                     145


gcc tca tac tca ggg gct tat tat gca cct ggt tat act cag acc agt    534
Ala Ser Tyr Ser Gly Ala Tyr Tyr Ala Pro Gly Tyr Thr Gln Thr Ser
    150                     155                     160


tac tcc aca gaa gtt cca agt act tac cgt tca tct ggc aac agc cca    582
Tyr Ser Thr Glu Val Pro Ser Thr Tyr Arg Ser Ser Gly Asn Ser Pro
165                     170                     175                 180


act cca gtc tct cgt tgg atc tat ccc cag cag gac tgt cag act gaa    630
Thr Pro Val Ser Arg Trp Ile Tyr Pro Gln Gln Asp Cys Gln Thr Glu
                185                     190                     195


gca ccc cct ctt agg ggg cag gtt cca gga tat ccg cct tca cag aac    678
Ala Pro Pro Leu Arg Gly Gln Val Pro Gly Tyr Pro Pro Ser Gln Asn
```

```
cct gga atg acc ctg ccc cat tat cct tat gga gat ggt aat cgt agt    726
Pro Gly Met Thr Leu Pro His Tyr Pro Tyr Gly Asp Gly Asn Arg Ser
        215                 220                 225

gtt cca caa tca gga ccg act gta cga cca caa gaa gat gcg tgg gct    774
Val Pro Gln Ser Gly Pro Thr Val Arg Pro Gln Glu Asp Ala Trp Ala
        230                 235                 240

tct cct ggt gct tat gga atg ggt ggc cgt tat ccc tgg cct tca tca    822
Ser Pro Gly Ala Tyr Gly Met Gly Gly Arg Tyr Pro Trp Pro Ser Ser
245                 250                 255                 260

gcg ccc tca gca cca ccc ggc aat ctc tac atg act gaa agt act tca    870
Ala Pro Ser Ala Pro Pro Gly Asn Leu Tyr Met Thr Glu Ser Thr Ser
                    265                 270                 275

cca tgg cct agc agt ggc tct ccc cag tca ccc cct tca ccc cca gtc    918
Pro Trp Pro Ser Ser Gly Ser Pro Gln Ser Pro Pro Ser Pro Pro Val
                280                 285                 290

cag cag ccc aag gat tct tca tac ccc tat agc caa tca gat caa agc    966
Gln Gln Pro Lys Asp Ser Ser Tyr Pro Tyr Ser Gln Ser Asp Gln Ser
                295                 300                 305

atg aac cgg cac aac ttt cct tgc agt gtc cat cag tac gaa tcc tcg   1014
Met Asn Arg His Asn Phe Pro Cys Ser Val His Gln Tyr Glu Ser Ser
            310                 315                 320

ggg aca gtg atc aat gaa gat tca gat ctt ttg gat tcc caa gtc cag   1062
Gly Thr Val Ile Asn Glu Asp Ser Asp Leu Leu Asp Ser Gln Val Gln
325                 330                 335                 340

tat agt gct gag cct cag ctg tat ggt aat gcc acc agt gac cat ccc   1110
Tyr Ser Ala Glu Pro Gln Leu Tyr Gly Asn Ala Thr Ser Asp His Pro
                    345                 350                 355

aac aat caa gat caa agt agc agt ctt cct gaa gaa tgt gta cct tca   1158
Asn Asn Gln Asp Gln Ser Ser Ser Leu Pro Glu Glu Cys Val Pro Ser
                360                 365                 370

gat gaa agt act cct ccg agt att aaa aaa atc ata cat gtg ctg gag   1206
Asp Glu Ser Thr Pro Pro Ser Ile Lys Lys Ile Ile His Val Leu Glu
                375                 380                 385

aag gtc cag tat ctt gaa caa gaa gta gaa gaa ttt gta gga aaa aag   1254
Lys Val Gln Tyr Leu Glu Gln Glu Val Glu Glu Phe Val Gly Lys Lys
```

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aca gac aaa gca tac tgg ctt ctg gaa gaa atg cta acc aag gaa ctt   1302
Thr Asp Lys Ala Tyr Trp Leu Leu Glu Glu Met Leu Thr Lys Glu Leu
405                 410                 415                 420

ttg gaa ctg gat tca gtt gaa act ggg ggc cag gac tct gta cgg cag   1350
Leu Glu Leu Asp Ser Val Glu Thr Gly Gly Gln Asp Ser Val Arg Gln
                425                 430                 435

gcc aga aaa gag gct gtt tgt aag att cag gcc ata ctg gaa aaa tta   1398
Ala Arg Lys Glu Ala Val Cys Lys Ile Gln Ala Ile Leu Glu Lys Leu
                440                 445                 450

gaa aaa aaa gga tta tga aaggatttag aacaaagtgg aagcctgtta           1446
Glu Lys Lys Gly Leu
          455

ctaacttgac caaagaacac ttgattaggt taattaccct ctttttgaaa tgcctgttga   1506

tgacaagaag caatacattc cagcttttcc tttgatttta tacttgaaaa actggcaaag   1566

gaatggaaga atattttagt catgaagttg ttttcagttt tcagacgaat gaatgtaata   1626

ggaaactatg gagttaccaa tattgccaag tagactcact ccttaaaaaa tttatggata   1686

tctacaagct gcttattacc agcaggaggg aaacacactt cacacaacag gcttatcaga   1746

aacctaccag atgaaactgg atataatttg agacaaacag gatgtgtttt tttaaacatc   1806

tggatatctt gtcacatttt tgtacattgt gactgctttc aacatatact tcatgtgtaa   1866

ttatagctta gactttagcc ttcttggact tctgttttgt tttgttattt gcagtttaca   1926

aatatagtat tattctctaa aaaaaaaaaa aaaaaaaaaa                         1966
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<210> 22
<211> 457
<212> PRT
<213> Homo sapiens

<400> 22
Met Ser Ala Leu Arg Arg Ser Gly Tyr Gly Pro Ser Asp Gly Pro Ser
1               5                   10                  15

Tyr Gly Arg Tyr Tyr Gly Pro Gly Gly Gly Asp Val Pro Val His Pro
            20                  25                  30
```

Pro Pro Pro Leu Tyr Pro Leu Arg Pro Glu Pro Pro Gln Pro Pro Ile
        35   40   45

Ser Trp Arg Val Arg Gly Gly Gly Pro Ala Glu Thr Thr Trp Leu Gly
        50   55   60

Glu Gly Gly Gly Gly Asp Gly Tyr Tyr Pro Ser Gly Gly Ala Trp Pro
    65   70   75   80

Glu Pro Gly Arg Ala Gly Gly Ser His Gln Glu Gln Pro Pro Tyr Pro
            85   90   95

Ser Tyr Asn Ser Asn Tyr Trp Asn Ser Thr Ala Arg Ser Arg Ala Pro
        100   105   110

Tyr Pro Ser Thr Tyr Pro Val Arg Pro Glu Leu Gln Gly Gln Ser Leu
        115   120   125

Asn Ser Tyr Thr Asn Gly Ala Tyr Gly Pro Thr Tyr Pro Pro Gly Pro
    130   135   140

Gly Ala Asn Thr Ala Ser Tyr Ser Gly Ala Tyr Tyr Ala Pro Gly Tyr
145   150   155   160

Thr Gln Thr Ser Tyr Ser Thr Glu Val Pro Ser Thr Tyr Arg Ser Ser
                165   170   175

Gly Asn Ser Pro Thr Pro Val Ser Arg Trp Ile Tyr Pro Gln Gln Asp
            180   185   190

Cys Gln Thr Glu Ala Pro Pro Leu Arg Gly Gln Val Pro Gly Tyr Pro
        195   200   205

Pro Ser Gln Asn Pro Gly Met Thr Leu Pro His Tyr Pro Tyr Gly Asp
        210   215   220

Gly Asn Arg Ser Val Pro Gln Ser Gly Pro Thr Val Arg Pro Gln Glu
225   230   235   240

Asp Ala Trp Ala Ser Pro Gly Ala Tyr Gly Met Gly Gly Arg Tyr Pro
            245   250   255

Trp Pro Ser Ser Ala Pro Ser Ala Pro Pro Gly Asn Leu Tyr Met Thr
            260   265   270

Glu Ser Thr Ser Pro Trp Pro Ser Ser Gly Ser Pro Gln Ser Pro Pro
    275   280   285

40

Ser Pro Pro Val Gln Gln Pro Lys Asp Ser Ser Tyr Pro Tyr Ser Gln
    290   295   300

Ser Asp Gln Ser Met Asn Arg His Asn Phe Pro Cys Ser Val His Gln
305   310   315   320

Tyr Glu Ser Ser Gly Thr Val Ile Asn Glu Asp Ser Asp Leu Leu Asp
                325   330   335

Ser Gln Val Gln Tyr Ser Ala Glu Pro Gln Leu Tyr Gly Asn Ala Thr
            340   345   350

Ser Asp His Pro Asn Asn Gln Asp Gln Ser Ser Ser Leu Pro Glu Glu
        355   360   365

Cys Val Pro Ser Asp Glu Ser Thr Pro Pro Ser Ile Lys Lys Ile Ile
    370   375   380

His Val Leu Glu Lys Val Gln Tyr Leu Glu Gln Glu Val Glu Glu Phe
385   390   395   400

Val Gly Lys Lys Thr Asp Lys Ala Tyr Trp Leu Leu Glu Glu Met Leu
                405   410   415

Thr Lys Glu Leu Leu Glu Leu Asp Ser Val Glu Thr Gly Gly Gln Asp
            420   425   430

Ser Val Arg Gln Ala Arg Lys Glu Ala Val Cys Lys Ile Gln Ala Ile
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Leu Glu Lys Leu Glu Lys Lys Gly Leu
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41

gcccagctcc ggtgccgcac cccgtaaagg gctgatcttc cacctcgcca cctcagccac 180

gggacgccaa gaccgcatcc aattcagact tcttttggtg cttgtgaaac tgaacacaac 240

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aaaagt atg gat atg gga aac caa cat cct tct att agt agg ctt cag       288
       Met Asp Met Gly Asn Gln His Pro Ser Ile Ser Arg Leu Gln
        1               5                       10

gaa atc caa aag gaa gta aaa agt gta gaa cag caa gtt atc ggc ttc      336
Glu Ile Gln Lys Glu Val Lys Ser Val Glu Gln Gln Val Ile Gly Phe
 15                  20                  25                  30

agt ggt ctg tca gat gac aag aat tac aag aaa ctg gag agg att cta      384
Ser Gly Leu Ser Asp Asp Lys Asn Tyr Lys Lys Leu Glu Arg Ile Leu
                 35                  40                  45

aca aaa cag ctt ttt gaa ata gac tct gta gat act gaa gga aaa gga     432
Thr Lys Gln Leu Phe Glu Ile Asp Ser Val Asp Thr Glu Gly Lys Gly
              50                  55                  60

gat att cag caa gct agg aag cgg gca gca cag gag aca gaa cgt ctt     480
Asp Ile Gln Gln Ala Arg Lys Arg Ala Ala Gln Glu Thr Glu Arg Leu
             65                  70                  75

ctc aaa gag ttg gag cag aat gca aac cac cca cac cgg att gaa ata     528
Leu Lys Glu Leu Glu Gln Asn Ala Asn His Pro His Arg Ile Glu Ile
    80                  85                  90

cag aac att ttt gag gaa gcc cag tcc ctc gtg aga gag aaa att gtg     576
Gln Asn Ile Phe Glu Glu Ala Gln Ser Leu Val Arg Glu Lys Ile Val
 95                  100                 105                 110

cca ttt tat aat gga ggc aac tgc gta act gat gag ttt gaa gaa ggc     624
Pro Phe Tyr Asn Gly Gly Asn Cys Val Thr Asp Glu Phe Glu Glu Gly
                 115                 120                 125

atc caa gat atc att ctg agg ctg aca cat gtt aaa act gga gga aaa     672
Ile Gln Asp Ile Ile Leu Arg Leu Thr His Val Lys Thr Gly Gly Lys
                 130                 135                 140

atc tcc ttg cgg aaa gca agg tat cac act tta acc aaa atc tgt gcg     720
Ile Ser Leu Arg Lys Ala Arg Tyr His Thr Leu Thr Lys Ile Cys Ala
             145                 150                 155

gtg caa gag ata atc gaa gac tgc atg aaa aag cag cct tcc ctg ccg     768
Val Gln Glu Ile Ile Glu Asp Cys Met Lys Lys Gln Pro Ser Leu Pro
    160                 165                 170
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42

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ctt tcc gag gat gca cat cct tcc gtt gcc aaa atc aac ttc gtg atg      816
Leu Ser Glu Asp Ala His Pro Ser Val Ala Lys Ile Asn Phe Val Met
175             180             185             190


tgt gag gtg aac aag gcc cga ggg gtc ctg att gca ctt ctg atg ggt      864
Cys Glu Val Asn Lys Ala Arg Gly Val Leu Ile Ala Leu Leu Met Gly
                195             200             205


gtg aac aac aat gag acc tgc agg cac tta tcc tgt gtg ctc tcg ggg      912
Val Asn Asn Asn Glu Thr Cys Arg His Leu Ser Cys Val Leu Ser Gly
                210             215             220


ctg atc gct gac ctg gat gct cta gat gtg tgc ggc cgg aca gaa atc      960
Leu Ile Ala Asp Leu Asp Ala Leu Asp Val Cys Gly Arg Thr Glu Ile
            225             230             235


aga aat tat cgg agg gag gta gta gaa gat atc aac aaa tta ttg aaa     1008
Arg Asn Tyr Arg Arg Glu Val Val Glu Asp Ile Asn Lys Leu Leu Lys
            240             245             250


tat ctg gat ttg gaa gag gaa gca gac aca act aaa gca ttt gac ctg     1056
Tyr Leu Asp Leu Glu Glu Glu Ala Asp Thr Thr Lys Ala Phe Asp Leu
255             260             265             270


aga cag aat cat tcc att tta aaa ata gaa aag gtc ctc aag aga atg     1104
Arg Gln Asn His Ser Ile Leu Lys Ile Glu Lys Val Leu Lys Arg Met
                275             280             285


aga gaa ata aaa aat gaa ctt ctc caa gca caa aac cct tct gaa ttg     1152
Arg Glu Ile Lys Asn Glu Leu Leu Gln Ala Gln Asn Pro Ser Glu Leu
                290             295             300


tac ctg agc tcc aaa aca gaa ttg cag ggt tta att gga cag ttg gat     1200
Tyr Leu Ser Ser Lys Thr Glu Leu Gln Gly Leu Ile Gly Gln Leu Asp
                305             310             315


gag gta agt ctt gaa aaa aac ccc tgc atc cgg gaa gcc agg aga aga     1248
Glu Val Ser Leu Glu Lys Asn Pro Cys Ile Arg Glu Ala Arg Arg Arg
                320             325             330


gca gtg atc gag gtg caa act ctg atc aca tat att gac ttg aag gag     1296
Ala Val Ile Glu Val Gln Thr Leu Ile Thr Tyr Ile Asp Leu Lys Glu
335             340             345             350


gcc ctt gag aaa aga aag ctg ttt gct tgt gag gag cac cca tcc cat     1344
Ala Leu Glu Lys Arg Lys Leu Phe Ala Cys Glu Glu His Pro Ser His
                355             360             365
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43

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aaa gcc gtc tgg aac gtc ctt gga aac ttg tct gag atc cag gga gaa   1392
Lys Ala Val Trp Asn Val Leu Gly Asn Leu Ser Glu Ile Gln Gly Glu
            370                 375                 380

gtt ctt tca ttt gat gga aat cga acc gat aag aac tac atc cgg ctg   1440
Val Leu Ser Phe Asp Gly Asn Arg Thr Asp Lys Asn Tyr Ile Arg Leu
        385                 390                 395

gaa gag ctg ctc acc aag cag ctg cta gcc ctg gat gct gtt gat ccg   1488
Glu Glu Leu Leu Thr Lys Gln Leu Leu Ala Leu Asp Ala Val Asp Pro
        400                 405                 410

cag gga gaa gag aag tgt aag gct gcc agg aaa caa gct gtg agg ctt   1536
Gln Gly Glu Glu Lys Cys Lys Ala Ala Arg Lys Gln Ala Val Arg Leu
415                 420                 425                 430

gcg cag aat att ctc agc tat ctc gac ctg aaa tct gat gaa tgg gag   1584
Ala Gln Asn Ile Leu Ser Tyr Leu Asp Leu Lys Ser Asp Glu Trp Glu
            435                 440                 445

tac tga aataccagag atctcacttt tgatactgtt ttgcacttca tatgtgcttc   1640
Tyr

tatgtataga gagctttcag ttcattgatt tatacgtgca tatttcagtc tcagtattta 1700

tgattgaagc aaattctatt cagtatctgc tgcttttgat gttgcaagac aaatatcatt 1760

acagcacgtt aacttttcca ttcggatcat tatctgtatg atgtggtgtg gtttgtttgg 1820

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taaatgggtt gtgcaagcat taaaatgcag gtctttcaga atctagaact aggcataacc 1940

ttacataata ctaggaaaat tatgagaaag gggaattttt ggttaaata agagtaaggt 2000

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44

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45

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            20                  25                  30

Leu Ser Asp Asp Lys Asn Tyr Lys Lys Leu Glu Arg Ile Leu Thr Lys
        35                  40                  45

Gln Leu Phe Glu Ile Asp Ser Val Asp Thr Glu Gly Lys Gly Asp Ile
    50                  55                  60

Gln Gln Ala Arg Lys Arg Ala Ala Gln Glu Thr Glu Arg Leu Leu Lys
65                  70                  75                  80

Glu Leu Glu Gln Asn Ala Asn His Pro His Arg Ile Glu Ile Gln Asn
                85                  90                  95

Ile Phe Glu Glu Ala Gln Ser Leu Val Arg Glu Lys Ile Val Pro Phe
            100                 105                 110

Tyr Asn Gly Gly Asn Cys Val Thr Asp Glu Phe Glu Glu Gly Ile Gln
            115                 120                 125
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46

Asp Ile Ile Leu Arg Leu Thr His Val Lys Thr Gly Gly Lys Ile Ser
    130   135   140

Leu Arg Lys Ala Arg Tyr His Thr Leu Thr Lys Ile Cys Ala Val Gln
145   150   155   160

Glu Ile Ile Glu Asp Cys Met Lys Lys Gln Pro Ser Leu Pro Leu Ser
                165   170   175

Glu Asp Ala His Pro Ser Val Ala Lys Ile Asn Phe Val Met Cys Glu
                180   185   190

Val Asn Lys Ala Arg Gly Val Leu Ile Ala Leu Leu Met Gly Val Asn
                195   200   205

Asn Asn Glu Thr Cys Arg His Leu Ser Cys Val Leu Ser Gly Leu Ile
    210   215   220

Ala Asp Leu Asp Ala Leu Asp Val Cys Gly Arg Thr Glu Ile Arg Asn
225   230   235   240

Tyr Arg Arg Glu Val Val Glu Asp Ile Asn Lys Leu Leu Lys Tyr Leu
                245   250   255

Asp Leu Glu Glu Glu Ala Asp Thr Thr Lys Ala Phe Asp Leu Arg Gln
                260   265   270

Asn His Ser Ile Leu Lys Ile Glu Lys Val Leu Lys Arg Met Arg Glu
    275   280   285

Ile Lys Asn Glu Leu Leu Gln Ala Gln Asn Pro Ser Glu Leu Tyr Leu
    290   295   300

Ser Ser Lys Thr Glu Leu Gln Gly Leu Ile Gly Gln Leu Asp Glu Val
305   310   315   320

Ser Leu Glu Lys Asn Pro Cys Ile Arg Glu Ala Arg Arg Arg Ala Val
                325   330   335

Ile Glu Val Gln Thr Leu Ile Thr Tyr Ile Asp Leu Lys Glu Ala Leu
                340   345   350

Glu Lys Arg Lys Leu Phe Ala Cys Glu Glu His Pro Ser His Lys Ala
                355   360   365

Val Trp Asn Val Leu Gly Asn Leu Ser Glu Ile Gln Gly Glu Val Leu
    370   375   380

47

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Ser Phe Asp Gly Asn Arg Thr Asp Lys Asn Tyr Ile Arg Leu Glu Glu
385             390             395             400

Leu Leu Thr Lys Gln Leu Leu Ala Leu Asp Ala Val Asp Pro Gln Gly
            405             410             415

Glu Glu Lys Cys Lys Ala Ala Arg Lys Gln Ala Val Arg Leu Ala Gln
        420             425             430

Asn Ile Leu Ser Tyr Leu Asp Leu Lys Ser Asp Glu Trp Glu Tyr
        435             440             445
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